

CLAIMS

We claim:

1. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

5 a) providing a first probe comprising:

- i) an upstream universal priming site (UUP);
- ii) an adapter sequence;
- iii) a first target-specific sequence comprising a first base at a readout position; and
- 10 iv) a downstream universal priming site (DUP);

b) contacting said first probe with said target sequence under conditions whereby only if said first base is perfectly complementary to a nucleotide at said detection position is a first hybridization complex formed;

c) removing non-hybridized first probes;

15 d) denaturing said hybridization complex;

e) amplifying said first probe to generate a plurality of amplicons;

f) contacting said amplicons with an array of capture probes; and

g) determining the nucleotide at said detection position.

20 2. A method according to claim 1 wherein said amplicons comprise a label.

3. A method according to claim 1 further comprising:

a) providing a second probe comprising:

- i) an upstream universal priming site (UUP);
- ii) an adapter sequence;
- 25 iii) a second target-specific sequence comprising a second base at said readout position; and
- iv) a downstream universal priming site (DUP);

b) contacting said second probe with said target sequence under conditions whereby only if said second base is perfectly complementary to a nucleotide at said detection position is a second hybridization complex formed;

30 c) removing non-hybridized second probes;

d) denaturing said second hybridization complex;

- e) amplifying said second probe to generate a plurality of amplicons;
- f) contacting said amplicons with an array of capture probes; and
- g) determining the nucleotide at said detection position.

✓ 5 4. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a plurality of readout probes each comprising:

- i) an upstream universal priming site (UUP);
- ii) an adapter sequence;
- iii) a target-specific sequence comprising a unique base at a readout position; and
- iv) a downstream universal priming site (DUP);

b) contacting said detection probes with said target sequence under conditions whereby only if said base at said readout position is perfectly complementary to a nucleotide at said detection position is a first hybridization complex formed;

c) removing non-hybridized first probes;

d) denaturing said first hybridization complex;

e) amplifying said detection probes to generate a plurality of amplicons;

f) contacting said amplicons with an array of capture probes; and

g) determining the nucleotide at said detection position.

Sub B4 20 5. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

a) hybridizing a first ligation probe to said first target domain, said first ligation probe comprising:

- i) an upstream universal priming site (UUP); and
- ii) a first target-specific sequence; and

b) hybridizing a second ligation probe to said second target domain, said second ligation probe comprising:

- i) a downstream universal priming site (DUP); and
- ii) a second target-specific sequence comprising a first base at an interrogation position;

wherein if said first base is perfectly complementary to said nucleotide at said

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- detection position a ligation complex is formed and wherein at least one of said first and second ligation probes comprises an adapter sequence;
- c) removing non-hybridized first probes;
 - d) providing a ligase that ligates said first and second ligation probes to form a ligated probe;
 - e) amplifying said ligated probe to generate a plurality of amplicons;
 - f) contacting said amplicons with an array of capture probes; and
 - g) determining the nucleotide at said detection position.

6. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

a) hybridizing a first ligation probe to said first target domain, said first ligation probe comprising:

- i) an upstream universal priming site (UUP); and
- ii) a first target-specific sequence; and

b) hybridizing a second ligation probe to said second target domain, said second ligation probe comprising:

- i) a downstream universal priming site (DUP); and
- ii) a second target-specific sequence comprising a first base at an interrogation position;

- wherein if said first base is perfectly complementary to said nucleotide at said detection position a ligation complex is formed and wherein at least one of said first and second ligation probes comprises an adapter sequence;
- c) removing non-hybridized first probes;
 - d) providing a ligase that ligates said first and second ligation probes to form a ligated probe;
 - e) hybridizing said ligated probe to a rolling circle (RC) sequence comprising:
 - i) an upstream priming sequence; and
 - ii) a downstream priming sequence;
 - f) providing a ligase that ligates said upstream and downstream priming sites to form a circular ligated probe;
 - g) amplifying said circular ligated probe to generate a plurality of amplicons;
 - f) contacting said amplicons with an array of capture probes; and
 - g) determining the nucleotide at said detection position.

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7. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

5 a) hybridizing a rolling circle (RC) probe to said target sequence, said RC probe comprising:

- 10 i) an upstream universal priming site (UUP); and
ii) a first target-specific sequence;
iii) a second target-specific sequence comprising a first base at an interrogation position, and
iv) an adapter sequence;

wherein if said first base is perfectly complementary to said nucleotide at said detection position a ligation complex is formed;

c) providing a ligase that ligates said first and second ligation probes to form a ligated probe;

15 d) amplifying said ligated probe to generate a plurality of amplicons;

e) contacting said amplicons with an array of capture probes; and

f) determining the nucleotide at said detection position.

8. A method according to claim 7, further comprising removing non-hybridized RC probe.

9. A method according to claim 1, 4, 5, 6 or 8 wherein said removing comprises:

- 20 a) enzymatically adding a binding ligand to said target sequence;
b) binding a hybridization complex comprising said target sequence comprising said binding ligand to a binding partner immobilized on a solid support;
c) washing away unhybridized probes; and
d) eluting said probe off said solid support.

25 10. A method according to claim 1, 4, 5, 6 or 8 wherein said removing is done using a double-stranded specific moiety.

11. A method according to claim 10 wherein said double-stranded specific moiety is an intercalator attached to a support.

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12. A method according to claim 9 wherein said support is a bead.

13. A method according to claim 1, 4, 5, 6 or 7 wherein said amplifying is done by:

- a) hybridizing a first universal primer to said UUP;
- b) providing a polymerase and dNTPs such that said first universal primer is extended;
- c) hybridizing a second universal primer to said DUP;
- d) providing a polymerase and dNTPs such that said second universal primer is extended; and
- e) repeating steps a) through d).

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14. A method according to claim 1, 4, 5, 6 or 7 wherein said array comprises:

- a) a substrate with a patterned surface comprising discrete sites; and
- b) a population of microspheres comprising at least a first subpopulation comprising a first capture probe and a second subpopulation comprising a second capture probe.

15. A method according to claim 14 wherein said discrete sites comprise wells.

16. A method according to claim 14 or 15 wherein said substrate comprises a fiber optic bundle.

17. A method of determining the identification of a nucleotide at a detection position in a genomic target sequence comprising:

- a) attaching a library of genomic target sequences to a solid support;
- b) adding at least one probe and an enzyme to form an extended primer;
- c) denaturing said extended primer from said target sequence;
- d) hybridizing said extended primer to an array comprising capture probes; and
- e) determining said nucleotide at said detection position.

18. A method according to claim 17 further comprising removing unhybridized probes.

19. A method according to claim 1, 4, 5, 6 or 7, further comprising providing a support on which the target sequence is immobilized.

20. A method according to claim 19, wherein said non-hybridized first probes are removed without

removing said target sequence from said support.

Sub A4 21. A method according to claim 1, 4, 5, 6 or 7, further comprising attaching said target sequence to a support.

Sub B7 22. A method according to claim 21, wherein said target sequence is attached to said support by a method selected from the group consisting of labeling said target sequence with a functional attachment moiety, absorption of said target sequence on a charged support, direct chemical attachment of said target sequence to said support and photocrosslinking said target sequence to said support.

Sub A5 23. A method according to claim 1, 4, 5, 6 or 7, wherein said support is selected from the group consisting of paper, plastic and tubes.

✓ 24. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a support on which the target sequence is immobilized;

b) providing a first probe comprising:

i) an upstream universal priming site (UUP);

ii) an adapter sequence;

iii) a first target-specific sequence comprising a first base at a readout position; and

iv) a downstream universal priming site (DUP);

c) contacting said first probe with said target sequence under conditions whereby only if said first base is perfectly complementary to a nucleotide at said detection position is a first hybridization complex formed;

d) removing non-hybridized first probes;

e) denaturing said hybridization complex;

f) amplifying said first probe to generate a plurality of amplicons;

g) contacting said amplicons with an array of capture probes; and

h) determining the nucleotide at said detection position

✓ 25. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

- 5
- a) providing a support on which the target sequence is immobilized;
- b) providing a plurality of readout probes each comprising:
- 5 i) an upstream universal priming site (UUP);
 - ii) an adapter sequence;
 - 10 iii) a target-specific sequence comprising a unique base at a readout position; and
 - iv) a downstream universal priming site (DUP);
- c) contacting said detection probes with said target sequence under conditions whereby only if said base at said readout position is perfectly complementary to a
- 10 nucleotide at said detection position is a first hybridization complex formed;
- d) removing non-hybridized first probes;
- e) denaturing said first hybridization complex;
- f) amplifying said detection probes to generate a plurality of amplicons;
- 15 g) contacting said amplicons with an array of capture probes; and
- h) determining the nucleotide at said detection position.

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26. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

- 20
- a) providing a support on which the target sequence is immobilized;
- b) hybridizing a first ligation probe to said first target domain, said first ligation probe comprising:
- 25 i) an upstream universal priming site (UUP); and
 - ii) a first target-specific sequence; and
- c) hybridizing a second ligation probe to said second target domain, said second ligation probe comprising:
- 25 i) a downstream universal priming site (DUP); and
 - ii) a second target-specific sequence comprising a first base at an interrogation position;

wherein if said first base is perfectly complementary to said nucleotide at said

30 detection position a ligation complex is formed and wherein at least one of said first and second ligation probes comprises an adapter sequence;

d) removing non-hybridized first probes;

e) providing a ligase that ligates said first and second ligation probes to form a ligated probe;

- f) amplifying said ligated probe to generate a plurality of amplicons;
- g) contacting said amplicons with an array of capture probes; and
- h) determining the nucleotide at said detection position.

✓ 5 27. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

- a) providing a support on which the target sequence is immobilized;
- b) hybridizing a first ligation probe to said first target domain, said first ligation probe comprising:

- i) an upstream universal priming site (UUP); and
- ii) a first target-specific sequence; and

- c) hybridizing a second ligation probe to said second target domain, said second ligation probe comprising:

- i) a downstream universal priming site (DUP); and
- ii) a second target-specific sequence comprising a first base at an interrogation position;

10 wherein if said first base is perfectly complementary to said nucleotide at said detection position a ligation complex is formed and wherein at least one of said first and second ligation probes comprises an adapter sequence;

- d) removing non-hybridized first probes;
- e) providing a ligase that ligates said first and second ligation probes to form a ligated probe;
- f) hybridizing said ligated probe to a rolling circle (RC) sequence comprising:

- i) an upstream priming sequence; and
- ii) a downstream priming sequence;

- g) providing a ligase that ligates said upstream and downstream priming sites to form a circular ligated probe;

- h) amplifying said circular ligated probe to generate a plurality of amplicons;
- i) contacting said amplicons with an array of capture probes; and
- j) determining the nucleotide at said detection position.

30 ✓ 28. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising a first target domain comprising said detection position and a second target domain adjacent to said detection position, wherein said method comprises:

a) providing a support on which the target sequence is immobilized;
b) hybridizing a rolling circle (RC) probe to said target sequence, said RC probe comprising:

- i) an upstream universal priming site (UUP); and
- ii) a first target-specific sequence;
- iii) a second target-specific sequence comprising a first base at an interrogation position; and
- iv) an adapter sequence;

wherein if said first base is perfectly complementary to said nucleotide at said detection position a ligation complex is formed;

- c) providing a ligase that ligates said first and second ligation probes to form a ligated probe;
- d) amplifying said ligated probe to generate a plurality of amplicons;
- e) contacting said amplicons with an array of capture probes; and
- f) determining the nucleotide at said detection position.

29. A method according to claim 28, further comprising removing unhybridized RC probe.

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